

10/019566

WO 01/02431

PCT/SE00/01390

531 Rec'd PCT/

31 DEC 2001

1

Sequence listing

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 <213> Homo sapiens
 <301> Hoppe HJ, Barlow PN, Reid KBM
 <302> A parallel three stranded α -helical bundle at the nucleation site of collagen triple-helix formation
 <303> FEBS Letters
 <304> 344
 <306> 191-195
 <307> 1994
 <400> 1

Pro Asp Val Ala Ser Leu Arg Gln Gln Val Glu Asp Leu Gln Gly
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Gln Val Gln His Ley Gln Ala Ala Phe Ser Gln Tyr Lys Lys Val
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Glu Leu Phe Pro Asn Gly
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<301> Harbury PB, Zhang T, Kim PS, Albert T
<302> A switch between two-, three-, and four-stranded coiled coils in GCN4 leucine zipper mutants
<303> Science
<304> 262
<306> 1401-1407
<307> 1993-11-26
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Met Lys Gln Ile Gly Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile Tyr His
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<301> Brinkmann U, Buchner J, Pastan I
<302> Independent domain folding of Pseudomonas exotoxin and single chain immunotoxins: Influence of interdomain connections
<303> Proc Natl Acad Sci US
<304> 89

<306> 3075-3079

<307> 1992

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<301> Brinkmann U, Buchner J, Pastan I

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<303> Proc Natl Acad Sci US

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- <301> Brinkmann U, Buchner J, Pastan I
- <302> Independent domain folding of Pseudomonas exotoxin and single chain immunotoxins: Influence of interdomain connections
- <303> Proc Natl Acad Sci US
- <304> 89
- <306> 3075-3079
- <307> 1992
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- <213> Homo sapiens

- <301> Dangi JL, Wensel TG, Morrison SL, Streier L, Herzenberg LA and Oi
T
- <302> Segmental flexibility and complement fixation of genetically
engineered chimeric human, rabbit and mouse antibodies
- <303> EMBO Journal
- <304> 7
- <306> 1989
- <307> 1988
- <400> 7
- Thr Pro Leu Gly Asp Thr Thr His Thr Ser Gly
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- <210> 8
- <211> 11
- <212> PRT
- <213> Adenovirus type 5
- <301> Stouten PFW, Sander C, Ruigrok WH, Cusack S
- <302> New triple-helical model for the shaft of the adenovirus fibre
- <303> Journal of molecular biology
- <304> 226
- <306> 1073-1084
- <307> 1992
- <400> 8
- Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
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<210> 9
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 <213> Simian virus 40
 <301> Fisher-Fantuzzi L and Vesco C 8:5495-5503, 1988
 <302> Cell-Dependent Efficiency of Reiterated Nuclear Signals in a Mutant
 Simian Virus 40 Oncoprotein Targeted to the Nucleus
 <303> Molecular Cell Biology
 <304> 8
 <306> 5495-5503
 <307> 1992
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 Tyr Leu Phe Trp Tyr Lys Gln Pro Pro Ser Gly Glu Leu Val Phe Leu Ile
 35 40 45

7

Arg Arg Asn Ser Phe Asp Glu Gln Asn Glu Ile Ser Gly Arg Tyr Ser
 50 55 60 65
 Trp Asn Phe Gln Lys Ser Thr Ser Ser Phe Asn Phe Thr Ile Thr Ala
 70 75 80
 Ser Gln Val Val Asp Ser Ala Val Tyr Phe Cys Ala Leu Gly Gly Val
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 Leu Ala Thr Gly Phe Phe Pro Asp His Val Glu Lys Ser Trp Trp
 35 40 45
 Val Asn Gly Lys Glu Val His Ser Gly Val Set Thr Asp Pro Gln Pro
 50 55 60
 Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser Ser
 65 70 75
 Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His Phe
 80 85 90
 Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr
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Tyr Trp Tyr Gln Gln Ser Leu Asp Gln Gly Leu Gln Phe Leu Ile His
 35             40             45
Tyr Tyr Asn Gly Glu Glu Arg Ala Lys Gly Asn Ile Leu Glu Arg Phe
50             55             60             65
Ser Ala Gln Gln Phe Pro Asp Leu His Ser Glu Leu Asn Leu Ser Ser
 70             75             80
Leu Glu Leu Gly Asp Ser Ala Leu Val Phe Cys Ala Ser Asn Ile Ala
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Leu

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<212> DNA

<213> Artificial sequence

<223> Sequence replacing the fiber gene sequence which was deleted between the NdeI restriction site in the fiber tail and the MunI site which begins at base 38 after the stop codon in the fiber. The sequence restores the NdeI and MunI sites and the wild type genome sequence between the fiber stop codon and the MunI site. In addition the added sequence contains an XhoI site allowing for the ligation of recombinant fibers.

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tatgcactcg agtaaagaat cgtttgtgtt atgtttcaac gtgtttatatt tc

<210> 14
 <211> 1746
 <212> DNA
 <213> Human adenovirus type 5
 <221> CDS
 <222> 1-1746
 <223> 1-129 Fiber tail
 130-1200 Fiber shaft
 1201-1746 Fiber knob
 <400> 14

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tat gac acg gaa acc ggt cct cca act gtg cct ttt ctt act cct ccc      96
Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr Pro Pro
             20             25             30
ttt gta tcc ccc aat ggg ttt caa gag agt ccc cct ggg gta ctc tct      144
Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
             35             40             45
ttg cgc cta tcc gaa cct cta gtt acc tcc aat ggc atg ctt gcg ctc      192
Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly Met Leu Ala Leu
             50             55             60
aaa atg ggc aac ggc ctc tct ctg gac gag gcc ggc aac ctt acc tcc      240
Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly Asn Leu Thr Ser
             65             70             75             80
caa aat gta acc act gtg agc cca cct ctc aaa aaa acc aag tca aac      288
Gln Asn Val Thr Thr Val Ser Pro Pro Leu Lys Lys Thr Lys Ser Asn
             85             90             95
ata aac ctg gaa ata tct gca ccc ctc aca gtt acc tca gaa gcc cta      336
Ile Asn Leu Glu Ile Ser Ala Pro Leu Thr Val Thr Ser Glu Ala Leu
             100            105            110
act gtg gct gcc gcc gca cct cta atg gtc gcg ggc aac aca ctc acc      384
Thr Val Ala Ala Ala Pro Leu Met Val Ala Gly Asn Thr Leu Thr
             115            120            125
atg caa tca cag gcc ccg cta acc gtg cac gac tcc aaa ctt agc att      432
Met Gln Ser Gln Ala Pro Leu Thr Val His Asp Ser Lys Leu Ser Ile
             130            135            140
gcc acc caa gga ccc ctc aca gtg tca gaa gga aag cta gcc ctg caa      480
Ala Thr Gln Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu Gln
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aca tca ggc ccc ctc acc acc acc gat agc agt acc ctt act atc act 528
 Thr Ser Gly Pro Leu Thr Thr Thr Asp Ser Ser Thr Leu Thr Ile Thr
 165 170 175
 gcc tca ccc cct cta act act gcc act ggt agc ttg ggc att gac ttg 576
 Ala Ser Pro Pro Leu Thr Thr Ala Thr Gly Ser Leu Gly Ile Asp Leu
 180 185 190
 aaa gag ccc att tat aca caa aat gga aaa cta gga cta aag tac ggg 624
 Lys Glu Pro Ile Tyr Thr Gln Asn Gly Lys Leu Gly Leu Lys Tyr Gly
 195 200 205
 gct cct ttg cat gta aca gac gac cta aac act ttg acc gta gca act 672
 Ala Pro Leu His Val Thr Asp Asp Leu Asn Thr Leu Thr Val Ala Thr
 210 215 220
 ggt cca ggt gtg act att aat aat act tcc ttg caa act aaa gtt act 720
 Gly Pro Gly Val Thr Ile Asn Asn Thr Ser Leu Gln Thr Lys Val Thr
 225 230 235 240
 gga gcc ttg ggt ttt gat tca caa ggc aat atg caa ctt aat gta gca 768
 Gly Ala Leu Gly Phe Asp Ser Gln Gly Asn Met Gln Leu Asn Val Ala
 245 250 255
 gga gga cta agg att gat tct caa aac aga cgc ctt ata ctt gat gtt 816
 Gly Gly Leu Arg Ile Asp Ser Gln Asn Arg Arg Leu Ile Leu Asp Val
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 agt tat ccg ttt gat gct caa aac caa cta aat cta aga cta gga cag 864
 Ser Tyr Pro Phe Asp Ala Gln Asn Gln Leu Asn Leu Arg Leu Gly Gln
 275 280 285
 ggc cct ctt ttt ata aac tca gcc cac aac ttg gat att aac tac aac 912
 Gly Pro Leu Phe Ile Asn Ser Ala His Asn Leu Asp Ile Asn Tyr Asn
 290 295 300
 aaa ggc ctt tac ttg ttt aca gct tca aac aat tcc aaa aag ctt gag 960
 Lys Gly Leu Tyr Leu Phe Thr Ala Ser Asn Asn Ser Lys Lys Leu Glu
 305 310 315 320
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 Val Asn Leu Ser Thr Ala Lys Gly Leu Met Phe Asp Ala Thr Ala Ile
 325 330 335
 gcc att aat gca gga gat ggg ctt gaa ttt ggt tca cct aat gca cca 1056
 Ala Ile Asn Ala Gly Asp Gly Leu Glu Phe Gly Ser Pro Asn Ala Pro
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 355 360 365
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 Ser Asn Lys Ala Met Val Pro Lys Leu Gly Thr Gly Leu Ser Phe Asp
 370 375 380
 agc aca ggt gcc att aca gta gga aac aaa aat aat gat aag cta act 1200
 Ser Thr Gly Ala Ile Thr Val Gly Asn Lys Asn Asn Asp Lys Leu Thr
 385 390 395 400
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 Leu Ala Thr Val Ser Val Leu Ala Val Lys Gly Ser Leu Ala Pro Ile
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 Ser Gly Thr Val Gln Ser Ala His Leu Ile Ile Arg Phe Asp Glu Asn
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 Gly Val Leu Leu Asn Asn Ser Phe Leu Asp Pro Glu Tyr Trp Asn Phe
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 Arg Asn Gly Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Gly Val Gly
 485 490 495
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 Phe Met Pro Asn Leu Ser Ala Tyr Pro Lys Ser His Gly Lys Thr Ala
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 Pro Val Thr Leu Thr Ile Thr Leu Asn Gly Thr Gln Glu Thr Gly Asp
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<212> PRT

<213> Mus musculus

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 35 40 45
 Ala Ala Ile Asn Ser Asp Gly Gly Ile Thr Tyr Tyr Leu Asp Thr Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
 65 70 75
 Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Leu Phe Tyr Cys
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<213> Mus musculus

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 65 70 75 80
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